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 04 2003
 08:30:15
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/055,877

DATE: 02/12/2003

TIME: 08:30:15

Input Set : D:\Cura551.app

Output Set: N:\CRF4\02112003\J055877.raw

3 <110> APPLICANT: DeCristofaro, Marc
 4 Padigaru, Muralidhara
 5 Miller, Charles
 6 Tchernev, Velizar
 7 Zhong, Mei
 8 Anderson, David
 9 Ballinger, Robert
 10 Gerlach, Valerie
 11 Spytek, Kimberly
 12 Ratelli, Luca
 13 Kekuda, Ramesh
 14 Guo, Xiaojia
 15 Zerhusen, Bryan
 16 Andrew, David
 17 Mezes, Peter
 18 Patturajan, Meera
 19 Burgess, Catherine
 20 Eisen, Andrew
 21 Wolenc, Adam
 22 Baumgartner, Jason
 23 Shimkets, Richard
 24 Gusev, Vladimir
 25 Vernet, Corine
 26 Taupier Jr., Raymond
 27 Pena, Carol
 28 Shenoy, Suresh
 29 Li, Li
 30 Casman, Stacie
 31 Boldog, Ference
 33 <120> TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
 35 <130> FILE REFERENCE: 21402-251
 37 <140> CURRENT APPLICATION NUMBER: 10/055877
 38 <141> CURRENT FILING DATE: 2002-01-22
 40 <150> PRIOR APPLICATION NUMBER: 60/262,892
 41 <151> PRIOR FILING DATE: 2001-01-19
 43 <150> PRIOR APPLICATION NUMBER: 60/263,598
 44 <151> PRIOR FILING DATE: 2001-01-23
 46 <150> PRIOR APPLICATION NUMBER: 60/263,799
 47 <151> PRIOR FILING DATE: 2001-01-24
 49 <150> PRIOR APPLICATION NUMBER: 60/264,117
 50 <151> PRIOR FILING DATE: 2001-01-25
 52 <150> PRIOR APPLICATION NUMBER: 60/264,139
 53 <151> PRIOR FILING DATE: 2001-01-25

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59 <151> PRIOR FILING DATE: 2001-01-30
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91 <150> PRIOR APPLICATION NUMBER: 60/291,701
92 <151> PRIOR FILING DATE: 2001-05-17
94 <150> PRIOR APPLICATION NUMBER: 60/296,960
95 <151> PRIOR FILING DATE: 2001-06-08
97 <160> NUMBER OF SEQ ID NOS: 512
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102 <211> LENGTH: 796
103 <212> TYPE: DNA
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107 <221> NAME/KEY: CDS
108 <222> LOCATION: (1)..(774)
109 <223> OTHER INFORMATION: no start codon
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112 agc aag ggc ttc ccc ata atc ctg gca ggc agg cct ccc ctg ggg ttt      48
113 Ser Lys Gly Phe Pro Ile Ile Leu Ala Gly Arg Pro Pro Leu Gly Phe
114   1               5               10               15
116 cca act tct gac ccc act gaa gtg ttt atc ctc ttc tct aac ccc agc      96
117 Pro Thr Ser Asp Pro Thr Glu Val Phe Ile Leu Phe Ser Asn Pro Ser
118           20           25           30
120 ctc ctt ttc cct gtc tcc atg tgc tct gag aga tgc tct gag aga tgc      144
121 Leu Leu Phe Pro Val Ser Met Cys Ser Glu Arg Cys Ser Glu Arg Cys
122       35       40       45
124 tcc cac tcc ccc agg ctc cct ctg cat ccc cct cat ttt ctt cct ccc      192

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125 Ser His Ser Pro Arg Leu Pro Leu His Pro Pro His Phe Leu Pro Pro
126      50      55      60
128 cag tgt gtc aat gga gtc ctg gcc ccc acc ctc tcg aca ttg tca cct 240
129 Gln Cys Val Asn Gly Val Leu Ala Pro Thr Leu Ser Thr Leu Ser Pro
130 65      70      75      80
132 ttt cct gat cca aag tgg gac ctt ctt ttc ccc caa gtg gtc ctg tct 288
133 Phe Pro Asp Pro Lys Trp Asp Leu Leu Phe Pro Gln Val Val Leu Ser
134      85      90      95
136 agg ggt gcc gct gcc ggg ccc cct ctg gtc ttc ctg ctg cag act ggg 336
137 Arg Gly Ala Ala Ala Gly Pro Pro Leu Val Phe Leu Leu Gln Thr Gly
138      100      105      110
140 gcc ttt tgg gag tca gca ggc gcc cgg gcc aac cgc agc cag cgt gag 384
141 Ala Phe Trp Glu Ser Ala Gly Ala Arg Ala Asn Arg Ser Gln Arg Glu
142      115      120      125
144 gcg agc gat gct tca ccg gcg agt cat cag ggt gag ctg gcc gtg tgc 432
145 Ala Ser Asp Ala Ser Pro Ala Ser His Gln Gly Glu Leu Ala Val Cys
146      130      135      140
148 gat gca gtc agt gtc tgg gtg aca gat ccc ggg act gct gtg gac ttg 480
149 Asp Ala Val Ser Val Trp Val Thr Asp Pro Gly Thr Ala Val Asp Leu
150 145      150      155      160
152 gtt gtg ctc gag gtg gag gtg ttg ggc gag gtg cct gca gct gtc ggc 528
153 Val Val Leu Glu Val Glu Val Leu Gly Glu Val Pro Ala Ala Val Gly
154      165      170      175
156 agt tcc ctc cac caa cac ttc ttt gtt gcc cac ttc gag gcc gat aac 576
157 Ser Ser Leu His Gln His Phe Phe Val Ala His Phe Glu Ala Asp Asn
158      180      185      190
160 tct gag gaa ggt ggc ccg ggg gta ggt gga ggg gct gcc gcc ggg gtg 624
161 Ser Glu Glu Gly Gly Pro Gly Val Gly Gly Gly Ala Ala Ala Gly Val
162      195      200      205
164 tgg acc ggg ggg cac tgg gtg tct gag tgc aag gcc aag cag tcc tat 672
165 Trp Thr Gly Gly His Trp Val Ser Glu Cys Lys Ala Lys Gln Ser Tyr
166      210      215      220
168 gtg cgg gca ttg acc gct gat gcc cag ggc cgt gtg gac tgg cga tgg 720
169 Val Arg Ala Leu Thr Ala Asp Ala Gln Gly Arg Val Asp Trp Arg Trp
170 225      230      235      240
172 att caa att ggc act gcc tgt gtc tgc aca ctc ctc agc cgg act ggc 768
173 Ile Gln Ile Gly Thr Ala Cys Val Cys Thr Leu Leu Ser Arg Thr Gly
174      245      250      255
176 cgg gcc tgagacccat gccaggaac tg 796
177 Arg Ala
180 <210> SEQ ID NO: 2
181 <211> LENGTH: 258
182 <212> TYPE: PRT
183 <213> ORGANISM: Homo sapiens
185 <400> SEQUENCE: 2
186 Ser Lys Gly Phe Pro Ile Ile Leu Ala Gly Arg Pro Pro Leu Gly Phe
187 1      5      10      15
189 Pro Thr Ser Asp Pro Thr Glu Val Phe Ile Leu Phe Ser Asn Pro Ser
190      20      25      30

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192 Leu Leu Phe Pro Val Ser Met Cys Ser Glu Arg Cys Ser Glu Arg Cys
193           35                40                45
195 Ser His Ser Pro Arg Leu Pro Leu His Pro Pro His Phe Leu Pro Pro
196           50                55                60
198 Gln Cys Val Asn Gly Val Leu Ala Pro Thr Leu Ser Thr Leu Ser Pro
199    65                70                75                80
201 Phe Pro Asp Pro Lys Trp Asp Leu Leu Phe Pro Gln Val Val Leu Ser
202           85                90                95
204 Arg Gly Ala Ala Ala Gly Pro Pro Leu Val Phe Leu Leu Gln Thr Gly
205           100               105               110
207 Ala Phe Trp Glu Ser Ala Gly Ala Arg Ala Asn Arg Ser Gln Arg Glu
208           115               120               125
210 Ala Ser Asp Ala Ser Pro Ala Ser His Gln Gly Glu Leu Ala Val Cys
211           130               135               140
213 Asp Ala Val Ser Val Trp Val Thr Asp Pro Gly Thr Ala Val Asp Leu
214   145                150                155                160
216 Val Val Leu Glu Val Glu Val Leu Gly Glu Val Pro Ala Ala Val Gly
217           165               170               175
219 Ser Ser Leu His Gln His Phe Phe Val Ala His Phe Glu Ala Asp Asn
220           180               185               190
222 Ser Glu Glu Gly Gly Pro Gly Val Gly Gly Gly Ala Ala Gly Val
223           195               200               205
225 Trp Thr Gly Gly His Trp Val Ser Glu Cys Lys Ala Lys Gln Ser Tyr
226           210               215               220
228 Val Arg Ala Leu Thr Ala Asp Ala Gln Gly Arg Val Asp Trp Arg Trp
229   225                230                235                240
231 Ile Gln Ile Gly Thr Ala Cys Val Cys Thr Leu Leu Ser Arg Thr Gly
232           245                250                255
234 Arg Ala
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240 <211> LENGTH: 1336
241 <212> TYPE: DNA
242 <213> ORGANISM: Homo sapiens
244 <220> FEATURE:
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250   Met Arg Ile Val Cys Leu Val Lys Asn Gln Gln Pro Leu Gly Ala
251     1                5                10                15
253 acc atc aag cgc cac gag atg aca ggg gac atc ttg gtg gcc agg atc      95
254 Thr Ile Lys Arg His Glu Met Thr Gly Asp Ile Leu Val Ala Arg Ile
255           20                25                30
257 atc cac ggt ggg ctg gcg gag aga agt ggg ttg cta tat gct gga gac      143
258 Ile His Gly Gly Leu Ala Glu Arg Ser Gly Leu Leu Tyr Ala Gly Asp
259           35                40                45
261 aaa ctg gta gaa gtg aat gga gtt tca gtt gag gga ctg gac cct gaa      191
262 Lys Leu Val Glu Val Asn Gly Val Ser Val Glu Gly Leu Asp Pro Glu
263           50                55                60

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265  caa  gtg  atc  cat  att  ctg  gcc  atg  tct  cga  ggc  aca  atc  atg  ttc  aag      239
266  Gln  Val  Ile  His  Ile  Leu  Ala  Met  Ser  Arg  Gly  Thr  Ile  Met  Phe  Lys
267      65              70              75
269  gtg  gtt  cca  gtc  tct  gac  cct  cct  gtg  aat  agc  cag  cag  atg  gta  aga      287
270  Val  Val  Pro  Val  Ser  Asp  Pro  Pro  Val  Asn  Ser  Gln  Gln  Met  Val  Arg
271  80              85              90              95
273  att  gtg  tac  gtc  cgt  gcc  atg  act  gag  tac  tgg  ccc  cag  gag  gat  ccc      335
274  Ile  Val  Tyr  Val  Arg  Ala  Met  Thr  Glu  Tyr  Trp  Pro  Gln  Glu  Asp  Pro
275      100              105              110
277  gac  atc  ccc  tgc  atg  gac  gct  gga  ttg  cct  ttc  cag  aag  ggg  gac  atc      383
278  Asp  Ile  Pro  Cys  Met  Asp  Ala  Gly  Leu  Pro  Phe  Gln  Lys  Gly  Asp  Ile
279      115              120              125
281  ctc  cag  att  gtg  gac  cag  aat  gat  gcc  ctc  tgg  tgg  cag  gcc  cga  aaa      431
282  Leu  Gln  Ile  Val  Asp  Gln  Asn  Asp  Ala  Leu  Trp  Trp  Gln  Ala  Arg  Lys
283      130              135              140
285  atc  tca  gac  cct  gct  acc  tgc  gct  ggg  ctt  gtc  cct  tct  aac  cac  ctt      479
286  Ile  Ser  Asp  Pro  Ala  Thr  Cys  Ala  Gly  Leu  Val  Pro  Ser  Asn  His  Leu
287      145              150              155
289  ctg  aag  agg  agg  aag  caa  cgg  gaa  ttc  tgg  tgg  tct  cag  ccg  tac  cag      527
290  Leu  Lys  Arg  Arg  Lys  Gln  Arg  Glu  Phe  Trp  Trp  Ser  Gln  Pro  Tyr  Gln
291  160              165              170              175
293  cct  cac  acc  tgc  ctc  aag  tca  acc  cta  caa  ctg  aag  gag  gag  ttt  gtt      575
294  Pro  His  Thr  Cys  Leu  Lys  Ser  Thr  Leu  Gln  Leu  Lys  Glu  Glu  Phe  Val
295      180              185              190
297  ggc  tac  ggt  cag  aag  ttc  ttt  ata  ggt  agg  tct  cac  ctc  agc  ccg  ctg      623
298  Gly  Tyr  Gly  Gln  Lys  Phe  Phe  Ile  Gly  Arg  Ser  His  Leu  Ser  Pro  Leu
299      195              200              205
301  cat  gcc  agt  gtg  tgc  tgc  acc  ggc  agc  tgc  tac  agt  gca  gtg  ggt  gcc      671
302  His  Ala  Ser  Val  Cys  Cys  Thr  Gly  Ser  Cys  Tyr  Ser  Ala  Val  Gly  Ala
303      210              215              220
305  cct  tac  gag  gag  gtg  gtg  agg  tac  cag  cga  cgc  cct  tca  gac  aag  tac      719
306  Pro  Tyr  Glu  Glu  Val  Val  Arg  Tyr  Gln  Arg  Arg  Pro  Ser  Asp  Lys  Tyr
307      225              230              235
309  cgc  ctc  ata  gtg  ctc  atg  ggt  atg  tcc  tta  gga  ccc  tct  ggt  gtt  gga      767
310  Arg  Leu  Ile  Val  Leu  Met  Gly  Met  Ser  Leu  Gly  Pro  Ser  Gly  Val  Gly
311  240              245              250              255
313  gta  aat  gag  ctc  aga  aga  caa  ctt  att  gaa  ttt  aat  ccc  agc  cat  ttt      815
314  Val  Asn  Glu  Leu  Arg  Arg  Gln  Leu  Ile  Glu  Phe  Asn  Pro  Ser  His  Phe
315      260              265              270
317  caa  agt  gct  gtg  cca  act  act  cgt  act  aaa  aag  agt  tac  gaa  atg  aat      863
318  Gln  Ser  Ala  Val  Pro  Thr  Thr  Arg  Thr  Lys  Lys  Ser  Tyr  Glu  Met  Asn
319      275              280              285
321  ggg  cgt  gag  tat  cac  tat  gtg  tcc  aag  gaa  aca  ttt  gaa  aac  ctc  ata      911
322  Gly  Arg  Glu  Tyr  His  Tyr  Val  Ser  Lys  Glu  Thr  Phe  Glu  Asn  Leu  Ile
323      290              295              300
325  tat  agt  cac  agg  agg  atg  ctg  gag  tat  ggt  gag  tac  aaa  ggc  cac  ctg      959
326  Tyr  Ser  His  Arg  Arg  Met  Leu  Glu  Tyr  Gly  Glu  Tyr  Lys  Gly  His  Leu
327      305              310              315
329  tat  ggc  act  agt  gtg  gat  gct  gtt  caa  aca  gtc  ctt  gtc  gaa  gga  aag      1007

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RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : D:\Cura551.app
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:43; N Pos. 6034,7262

Seq#:45; N Pos. 6016,7244

Seq#:51; N Pos. 6031,7259

Seq#:185; Xaa Pos. 205,211

VERIFICATION SUMMARY

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L:5523 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:6022
M:341 Repeated in SeqNo=43
L:6270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:5964
M:341 Repeated in SeqNo=45
L:7801 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51 after pos.:6029
M:341 Repeated in SeqNo=51
L:23162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:185 after pos.:192
M:341 Repeated in SeqNo=185